Amendments to the Specification:

Please add the following figure descriptions beginning at page 10, line 19:

--Fig. 10: Structure and sequences of the 2C TCR CDR3α. Alignment of amino acid sequences (SEQ ID NO:1-22) of mutant scTCRs isolated by yeast display and selection with QL9/L^d. Display plasmids were isolated from yeast clones after selection and sequenced to determine CDR3α sequences. Mutants m1, m2, m3, m4, m10 and m11 were isolated after the third round of sorting. All other mutants were isolated after the fourth round of sorting.

Fig. 11: SIYR/K^b Binders (3SQ2, 3SQ5): CDR3α Sequences. (SEQ ID NO:23-39)

Fig. 12: Alignment of VαCDR3 Mutant Sequences with High Affinity for dEV8/K^b (4d1, 4d2, 3Sd3, 3dS6, 3dS2, 3d2) and SIYR/K^b. (SEQ ID NO:40-47)

Fig. 13: Alignment of VβCDR3 Sequences of Mutant scTCRs Selected for High Affinity for QL9/L^d from a CDR3α Yeast Library. All have qL2 CDR3α (SHQGRYL (SEQ ID NO:13)). QB1/5=wt; QB3 not sequenced.-- (SEQ ID NO:48-63)

Please replace the paragraph beginning at page 16, line 1 with the following rewritten paragraph:

--CDR3α sequences of the fifteen mutants all differed from the starting 2C TCR sequence ~~(Table 1)~~ FIG 10. Comparison by a BLAST alignment algorithm aligned the sequences into two motifs. One motif contained glycine in the middle of the 5 residue stretch whereas the other motif contained three tandem prolines. Evidence that all three prolines are important in generating the highest affinity site is suggested by results with mutant q3r. Mutant q3r contained only two of the three prolines and exhibited reduced binding compared to the triple-proline mutants. The glycine-containing mutants appeared to have preferences for positive-charged residues among the two residues to the carboxy side (7/9) and aromatic and/or positive-charged residues among the two residues to the amino side (4/9 and 5/9). Without wishing to be bound by theory, it is believed that the selection for a glycine residue at position 102 in the motif indicates that the CDR3α loop requires conformational flexibility around this residue in order to achieve increased affinity. This is consistent with the large (6Å) conformational difference observed between the CDR3α loops of the liganded and unliganded TCR [Garcia et al. (1998) *supra*]. It is also interesting to note that glycine is the most common

residue at the V(D)J junctions of antibodies and that the presence of a glycine has recently been associated with increased affinity in the response to the (4-hydroxy-3-nitrophenyl) acetyl hapten [Furukawa et al. (1999) *Immunity* 11:329-338].--

Please replace the paragraph beginning at page 32, line 24 with the following rewritten paragraph:

--Using the same library of yeast-displayed mutants of the CDR3α region of the TCR, it was possible to select for higher affinity TCRs that are specific for yet a different peptide bound to a different MHC molecule. In this case the peptide called SIYR (SIYRYYGL (SEQ ID NO:5)) was bound to the MHC molecule called K^b, and this ligand complex was used in fluorescent form to select by flow cytometry. Sixteen clones expressing high affinity TCR were sequenced, each showing a different sequence in the CDR3α region ~~(Table 2)~~ FIG 11.--

Please replace the paragraph beginning at page 33, line 23 with the following rewritten paragraph:

--Six of the clones that were isolated by selection with dEV8/K^b were sequenced and the CDR3 sequences all differed ~~(Table 3)~~FIG 12. These sequences were similar in sequence, but different from, those isolated by selection with SIYR/K^b (two examples, 3SQ2 and 3SQ5, are also shown in ~~Table 3)~~FIG 12. It can be concluded that it is possible to isolate higher affinity TCRs against different antigens, even using the same TCR library of mutants.--

Please cancel the Tables on pages 35-38.